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TCTCACGACCTGCTGGAGACTGGACGCCACACCTGACCCGAACTCGGAGGC GTGCTCCTCACCCGCCGGCTAGCA
GCCCGGGCCCTGAGCTCCCGCCGACGCCGCTGGGGGGCCGACAGGCCCTCGGCCTGATGCTGAGTGGATCGAGG
GCCCGGGGGCGGGCGGGAGTACGGGCCTCTGGCGCCTAGGCCAGCCGAGGTGTGGTCTTAGGCTCTCAGGCTCG
CTAGCTCCCGCCCCGGCTGGATGGCTCCCTGCCATAAATGTGGCTGCTGAGGCCGGTGGCGTGGCCGTGGCCCGT CG
CGCTGCTGCTGCCGCTCCAAGTCATCTCCGCCCCGGCTCTCCCTGCCACCTCGGGCTGCCACCCGCTCC

M D K I L E G L V S S SEQ ID NO:2
TTATCCCCCTGGCCCTGGCCTTGCAGCGTGGCGACA ATG GAC AAG ATC CTG GAG GGC CTT GTG AGT TCC 33
↑SEQ ID NO:3→

S H P L P L K R V I V R K V V E S A E H 31
TCG CAT CCC CTG CCC CTC AAG CGG GTG ATT GTG CGG AAG GTG GTG GAA TCG GCG GAG CAC 93

W L D E A Q C E A M F D L T T R L I L E 51
TGG CTA GAC GAG GCG CAG TGC GAG GCC ATG TTT GAC CTG ACG ACC CGG CTC ATC CTG GAG 153

G Q D P F Q R Q V G H Q V L E A Y A R Y 71
GGC CAG GAC CCT TTC CAG CGG CAG GTG GGG CAC CAG GTG CTG GAG GCC TAC GCA CGA TAC 213

H R P E F E S F F N K T F V L G L L H Q 91
CAC CGG CCA GAG TTC GAG TCC TTC AAC AAG ACC TTC GTG TTG GGC CTC CTT CAT CAG 273

G Y H S L D R K D V A I L D Y I H N G L 111
GGC TAC CAC TCT CTG GAC AGG AAG GAT GTA GCC ATC CTG GAC TAC ATT CAC AAC GGC CTG 333

K L I M S C P S V L D L F S L L Q V E V 131
AAG CTG ATT ATG AGC TGT CCG TCG GTG CTG GAT CTC TTT AGC CTC CTG CAG GTA GAG GTG 393

L R M V C E R P E P Q L C A R L S D L L 151
TTA CGG ATG GTG TGT GAG AGG CCG GAG CCG CAG CTC TGT GCC CGA CTG AGC GAC CTT CTG 453

T D F V Q C I P K G K L S I T F C Q Q L 171
ACC GAC TTT GTG CAA TGC ATC CCC AAG GGG AAA TTG TCC ATC ACG TTC TGT CAA CAG CTG 513

V R T I G H F Q C V S T Q E R E L R E Y 191
GTT CGA ACG ATA GGC CAT TTC CAG TGC GTG TCC ACC CAG GAA AGA GAG CTG C GAA TAT 573

V S Q V T K V S N L L Q N I W K A E P A 211
GTC TCC CAG GTG ACA AAA GTG AGT AAC TTG CTG CAG AAC ATC TGG AAG GCC GAG CCT GCC 633

T L L P S L Q E V F A S I S S T D S F 231
ACA CTA CTG CCT TCC CTG CAA GAA GTT TTT GCA AGC ATC TCT TCC ACA GAT G TCA TTT 693

E P S V A L A S L V Q H I P L Q M I T V 251
GAA CCT TCT GTA GCA TTG GCA AGC CTT GTG CAG CAT ATT CCT CTT CAG ATG ATT ACA GTT 753

L I R S L T T D P N V K D A S M T Q A L 271

FIG 1A

CTC ATC AGG AGC CTT ACT ACG GAT CCA AAT GTA AAA GAT GCA AGT ATG ACC CAA GCC CTT	813
C R M I D W L S W P L A Q H V D T W V I	291
TGC AGA ATG ATT GAC TGG CTA TCC TGG CCA TTG GCT CAG CAT GTG GAT ACA TGG GTA ATT	873
A L I K G L A A V Q K F T I L I D V T L	311
GCA CTC CTG AAA GGA CTG GCA GCT GTC CAG AAG TTT ACT ATT TTG ATA GAT GTT ACT TTG	933
L K I E L V F N R L W F P L V R P G A L	331
CTG AAA ATA GAA CTG GTT TTT AAT CGA CTT TGG TTT CCT CTT GTG AGA CCT GGT GCT CTT	993
A V L S H M L L S F Q H S P E A F H L I	351
GCA GTT CTT TCT CAC ATG CTG CTT AGC TTT CAG CAT TCT CCA GAG GCG TTC CAT TTG ATT	1053
V P H V V N L V H S F K N D G L P S S T	371
GTT CCT CAT GTG GTT AAT TTG GTT CAT TCT TTC AAA AAT GAT GGT CTG CCT TCA AGT ACA	1113
A F L V Q L T E L I H C M M Y H Y S G F	391
GCC TTC TTA GTA CAA TTA ACA GAA TTG ATA CAC TGT ATG ATG TAT CAT TAT TCT GGA TTT	1173
P D L Y E P I L E A I K D F P K P S E E	411
CCA GAT CTC TAT GAA CCT ATT CTG GAG GCA ATA AAG GAT TTT CCT AAG CCC AGT GAA GAG	1233
K I K L I L N Q S A W T S Q S N S L A S	431
AAG ATT AAG TTA ATT CTC AAT CAA AGT GCC TGG ACT TCT CAA TCC AAT TCT TTG GCG TCT	1293
C L S R L S G K S E T G K T G L I N L G	451
TGC TTG TCT AGA CTT TCT GGA AAA TCT GAA ACT GGG AAA ACT GGT CTT ATT AAC CTA GGA	1353
N T C Y M N S V I Q A L F M A T D F R R	471
AAT ACA TGT TAT ATG AAC AGT GTT ATA CAA GCC TTG TTT ATG GCC ACA GAT TTC AGG AGA	1413
Q V L S L N L N G C N S L M K K L Q H L	491
CAA GTA TTA TCT TTA AAT CTA AAT GGG TGC AAT TCA TTA ATG AAA AAA TTA CAG CAT CTT	1473
F A F L A H T Q R E A Y A P R I F F E A	511
TTT GCC TTT CTG GCC CAT ACA CAG AGG GAA GCA TAC GCA CCT CGG ATA TTC TTT GAG GCT	1533
S R P P W F T P R S Q Q D C S E Y L R F	531
TCC AGA CCT CCA TGG TTT ACT CCC AGA TCA CAG CAA GAC TGT TCT GAA TAC CTC AGA TTT	1593
L L D R L H E E E K I L K V Q A S H K P	551
CTC CTT GAC AGG CTC CAT GAA GAA AAG ATC TTG AAA GTT CAG GGC TCA CAC AAG CCT	1653
S E I L E C S E T S L Q E V A S K A A V	571
TCT GAA ATT CTG CAA TGC AGT GAA ACT TCT TTA CAG GAA GTA GCT AGT AAA GCA GCA GTA	1713
L T E T P R T S D G E K T L I E K M F G	591
CTA ACA GAG ACC CCT CGT ACA AGT GAC GGT GAG AAG ACT TTA ATA GAA AAA ATG TTT GGA	1773
G K L R T H I R C L N C R S T S Q K V E	611
GGA AAA CTA CGA ACT CAC ATA CGT TGT TTG AAC TGC AGG AGT ACC TCA CAA AAA GTG GAA	1833
A F T D L S L A F C P S S S L E N M S V	631
GCC TTT ACA GAT CTT TCG CTT GCC TTT TGT CCT TCC TCT TCT TTG GAA AAC ATG TCT GTC	1893
Q D P A S S P S I Q D G G L M Q A S V P	651

FIG 1B

CAA GAT CCA GCA TCA TCA CCC AGT ATA CAA GAT GGT GGT CTA ATG CAA GCC TCT GTA CCC	1953
G P S E E P V V Y N P T T A A F I C D S	671
GGT CCT TCA GAA GAA CCA GTA GTT TAT AAT CCA ACA ACA GCT GCC TTC ATC TGT GAC TCA	2013
L V N E K T I G S P P N E F Y C S E N T	691
CTT GTG AAT GAA AAA ACC ATA GGC AGT CCT CCT AAT GAG TTT TAC TGT TCT GAA AAC ACT	2073
S V P N E S N K I L V N K D V P Q K P G	711
TCT GTC CCT AAC GAA TCT AAC AAG ATT CTT GTT AAT AAA GAT GTA CCT CAG AAA CCA GGA	2133
G E T T P S V T D L L N Y F L A P E I L	731
GGT GAA ACC ACA CCT TCA GTA ACT GAC TTA CTA AAT TAT TTT TTG GCT CCA GAG ATT CTT	2193
T G D N Q Y Y C E N C A S L Q N A E K T	751
ACT GGT GAT AAC CAA TAT TAT TGT GAA AAC TGT GCC TCT CTG CAA AAT GCT GAG AAA ACT	2253
M Q I T E E P E Y L I L T L L R F S Y D	771
ATG CAA ATC ACG GAG GAA CCT GAA TAC CTT ATT CTT ACT CTC CTG AGA TTT TCA TAT GAT	2313
Q K Y H V R R K I L D N V S L P L V L E	791
CAG AAG TAT CAT GTG AGA AGG AAA ATT TTA GAC AAT GTA TCA CTG CCA CTG GTT TTG GAG	2373
L P V K R I T S F S S L S E S W S V D V	811
TTG CCA GTT AAA AGA ATT ACT TCT TTC TCT TCA TTG TCA GAA AGT TGG TCT GTA GAT GTT	2433
D F T D L S E N L A K K L K P S G T D E	831
GAC TTC ACT GAT CTT AGT GAG AAC CTT GCT AAA AAA TTA AAG CCT TCA GGG ACT GAT GAA	2493
A S C T K L V P Y L L S S V V V H S G I	851
GCT TCC TGC ACA AAA TTG GTG CCC TAT CTA TTA AGT TCC GTG GTT CAC TCT GGT ATA	2553
S S E S G H Y Y S Y A R N I T S T D S S	871
TCC TCT GAA AGT GGG CAT TAC TAT TCT TAT GCC AGA AAT ATC ACA AGT ACA GAC TCT TCA	2613
Y Q M Y H Q S E A L A L A S S Q S H L L	891
TAT CAG ATG TAC CAC CAG TCT GAG GCT CTG GCA TTA GCA TCC TCC CAG AGT CAT TTA CTA	2673
G R D S P S A V F E Q D L E N K E M S K	911
GGG AGA GAT AGT CCC AGT GCA GTT TTT GAA CAG GAT TTG GAA AAT AAG GAA ATG TCA AAA	2733
E W F L F N D S R V T F T S F Q S V Q K	931
GAA TGG TTT TTA TTT AAT GAC AGT AGA GTG ACA TTT ACT TCA TTT CAG TCA GTC CAG AAA	2793
I T S R F P K D T A Y V L L Y K K Q H S	951
ATT ACG AGC AGG TTT CCT AAG GAC ACA GCT TAT GTG CTT TTG TAT AAA AAA CAG CAT AGT	2853
T N G L S G N N P T S G L W I N G D P P	971
ACT AAT GGT TTA AGT GGT AAT AAC CCA ACC AGT GGA CTC TGG ATA AAT GGA GAC CCA CCT	2913
L Q K E L M D A I T K D N K L Y L Q E Q	991
CTA CAG AAA GAA CTT ATG GAT GCT ATA ACA AAA GAC AAT AAA CTA TAT TTA CAC GAA CAA	2973
E L N A R A R A L Q A A S A S C S F R P	1011
GAG TTG AAT GCT CGA GCC CGG GCC CTC CAA GCT GCA TCT GCT TCA TGT TCA TTT CGG CCC	3033
N G F D D N D P P G S C G P T G G G G G	1031

FIG 1C

AAT GGA TTT GAT GAC AAC GAC CCA CCA GGA AGC TGT GGA CCA ACT GGT GGA GGG GGT GGA	3093
G G F N T V G R L V F *	1043
GGA GGA TTT AAT ACA GTT GGC AGA CTC GTA TTT TGA	3129
←SEQ ID NO:3↑	
TCCTGAGAGAGTCCAAAATGCACTGGTCACGAAACGTCTAATACTATGACTGTTAAAATGTCAGACTATAACAAATATC	
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TGTTCAGAAGAAAATATGTACCTGGTCCCTAATTAAGCTCGTTAAATTGGTAGAAGCATTAAATGGCTATCTCA	
GTTTACTGAACAAAAATGTAATTATTAGCATTCTTATAAAAGAATTGATGCTAGAGGTAAAAAAATACTTGT	
TTTAAAAAAATCCTTACGTCTGTGTAATTACCCCATTATTAATTCAAGTCCTGAAAATCAACTAGAGATTATAAA	
GTCTCTAAAGAAGGCAATAACAAAATTATCAAGATATAGTACTTTCAGTTTGTGTTAGTGTCTTCAGCATCACTGT	
GTCTGTATTCAGTACAATGTTTAAAAAGGATTCTTATACATATGTGCTGAATTGATTAAAGGAAAGTTGCAT	
GATCCTGTAGGAGAACATTTACCTAAAAATGCTAACCTTATAGTATTCTAATTGTTCAAGGATTAAATTCT	
GATCCTGTAGGAGAACATTTACCTAAAAATGCTAACCTTATAGTATTCTAATTGTTCAAGGATTAAATTCT	

FIG 1D

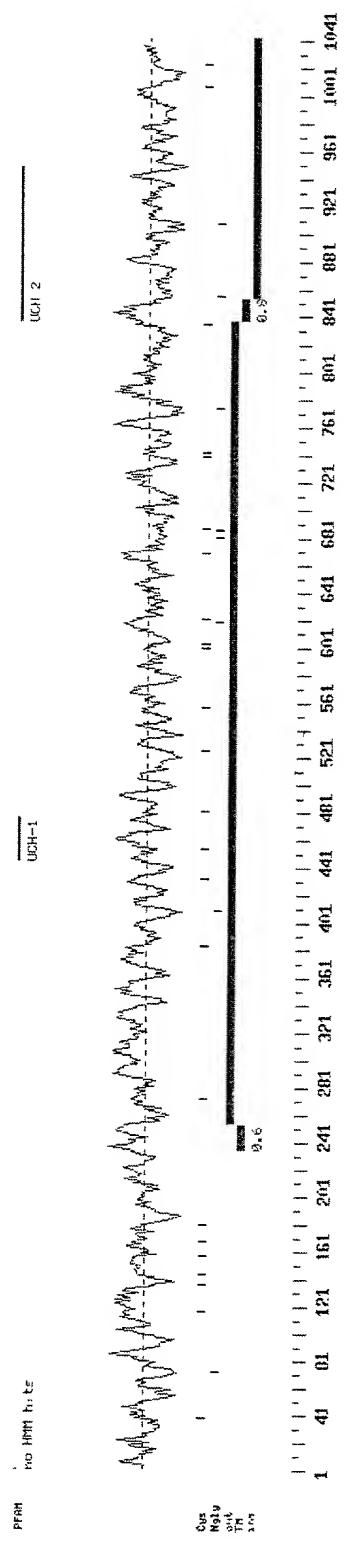


Fig. 2

->tGLiN1GNTCYmNSvLQcLfssipplrdy1ldi<- SEQ ID NO:4
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23430 445 TGLINLGNTCYMNSVIQALFMATDFRRQVLSL 476

Fig. 3

*->gpgkYeLyaVvvHsGss1sgGHYtayvkken..... SEQ ID NO:5
+ + Y L +VvvHsG s+ +GHY++y+++ +++++ + +++++
23430 836 KLPYLLSSVVVHSGISSEGHYSYARNITstdssyqmyhqseala 882
..... WykFDDdkVsrvteeevlke
+++++ ++++++ +++ ++++ +++W++F+D++V+ + v+k
23430 883 lassqshllgrdpsavfeqdlenkemskeWFLFNDSRVTFTSFQSVQKI 932
sggesgdtsAYiLfYer<-*
+ ++AY+L+Y++
23430 933 TSR--FPKDTAYVLLYKK 948

Fig. 4

Query: 710 PGGETPSVTDLLNYFLAPEILTGDNQYYCENCASLQNAEKTMQITEEPEYLILTLRFS 769 SEQ ID
NO:6
P G+ + S+ D L F PE L GDN+Y+CE C Q+A K + I + P+ L + L RF
Sbjct: 12 PEGDHS-SLEDCLEQFFKPEELEGDNKYHCEKCKKQDATKQLTIKKLPQVLTIHLKRFE 70

Fig. 5